

## AMENDMENTS TO THE CLAIMS

The following listing of claims replaces all prior versions of claims in the application:

### *Listing of Claims:*

1. (Currently amended) A method for detecting *in vivo* CCI-779 activity in a patient having a solid tumor, the method comprising:
  - (a) generating an expression profile of at least one CCI-779 activity gene selected from Table 5 in a peripheral blood sample obtained from the patient having the solid tumor and at a stage of treatment with CCI-779;
  - (b) ~~comparing an~~ the expression profile of said at least one CCI-779 activity gene generated in step (a) ~~in a peripheral blood sample of a patient~~ to a reference expression profile of said at least one CCI-779 activity gene[[],]; and
  - (c) detecting *in vivo* CCI-779 activity in the patient based on the comparison result from step (b), wherein a statistically significant change in the expression profile of said at least one CCI-779 activity gene compared to the reference expression profile is indicative of the *in vivo* CCI-779 activity ~~wherein said at least one gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients who have a non-blood disease and are subject to a drug therapy as compared to PBMCs isolated from said patients before said drug therapy, and wherein the patient has the non-blood disease and is being treated by said drug therapy.~~
2. (Canceled)
3. (Canceled)
4. (Currently amended) The method according to claim 13, wherein the solid tumor is renal cell carcinoma (RCC).
5. (Canceled)
6. (Withdrawn-currently amended) The method according to claim 12, wherein said at least one CCI-779 activity gene includes at least two genes selected from Table 5.
7. (Original) The method according to claim 1, wherein the peripheral blood sample is a whole blood sample.

8. (Canceled)

9. (Currently amended) The method according to claim 1, wherein the expression profile of the at least one CCI-779 activity gene generated in step (a) is determined by reverse-transcription polymerase chain reaction (RT-PCR) or immunoassays.

10. (Currently amended) The method according to claim 1, wherein the reference expression profile is a baseline~~an average~~ expression profile of said at least one CCI-779 activity gene in a peripheral blood samples isolated from said patients before CCI-779 treatmentsaid drug therapy.

11. (Currently amended) The method according to claim 1, wherein the reference expression profile is an reference expression profile of said at least one CCI-779 activity gene in a reference peripheral blood sample isolated from the patient beforeat a different stage of CCI-779 treatmentsaid drug therapy.

12-16. (Canceled)

17. (Currently amended) A method for identifying genes modulated by drugCCI-779activity genes, the method comprising:

(a) obtaining a peripheral blood sample from a patient having a solid tumor and at a stage of treatment with CCI-779;

(b) detectinggenerating an expression profile of genes in the peripheral blood sample obtained in step (a)s of patients who have a non blood disease and are subject to a drug therapy;  
and

(c) comparing said expression profile generated in step (b) to a referencebaseline expression profile of said genes in a reference peripheral blood samples isolated from said patients before said drug therapy so as to identify one or more differentially expressed genes drug activity genes whose expression levels in peripheral blood samples can be modulated by said drug therapy.

18. (Withdrawn) A kit comprising a plurality of polynucleotides, wherein each of said polynucleotides is capable of hybridizing under stringent or nucleic acid array hybridization conditions to an RNA transcript, or the complement thereof, of a different respective gene selected from Table 5.

19. (Withdrawn) A kit comprising a plurality of antibodies, wherein each of said antibodies is capable of binding to a polypeptide encoded by a different respective gene selected from Table 5.
20. (Withdrawn) A nucleic acid array comprising polynucleotide probes, wherein a substantial portion of all polypeptide probes on the nucleic acid array can hybridize under stringent or nucleic acid array hybridization conditions to RNA transcripts, or the complements thereof, of genes selected from Table 5.
21. (New) The method according to claim 1, wherein the at least one CCI-779 activity gene comprises profilin 1.
22. (New) The method according to claim 1, wherein the stage of treatment with CCI-779 is 8 weeks after initiation of CCI-779 treatment.
23. (New) The method according to claim 1, wherein the stage of treatment with CCI-779 is 16 weeks after initiation of CCI-779 treatment.
24. (New) The method according to claim 17, wherein the reference expression profile is a baseline expression profile of a peripheral blood sample obtained from said patient before CCI-779 treatment.
25. (New) The method according to claim 17, wherein the reference peripheral blood sample is obtained from said patient at a different stage of CCI-779 treatment.
26. (New) The method according to claim 17, wherein the stage of treatment with CCI-779 is 8 weeks after initiation of CCI-779 treatment.
27. (New) The method according to claim 17, wherein the stage of treatment with CCI-779 is 16 weeks after initiation of CCI-779 treatment.